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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- AA2
- (i) APPLICANT: TSUCHIYA, Masayuki
SATO, Koh
BENDIG, Mary
JONES, Steven
SALDANHA, Jose
 - (ii) TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
 - (iii) NUMBER OF SEQUENCES: 158
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Foley & Lardner
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 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20007-5109
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/137,117
 - (B) FILING DATE: 20-DEC-1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO PCT/JP92/00544
 - (B) FILING DATE: 24-APR-1992
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 4-32084
 - (B) FILING DATE: 19-FEB-1992
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 3-95476
 - (B) FILING DATE: 25-APR-1991
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: WEGNER, Harold C.
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG

40

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
ACTAGTCGAC ATGGAGWCAG ACACACTCCT GYTATGGGT

39

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
ACTAGTCGAC ATGAGTGTGC TCACTCAGGT CCTGGSGTTG

40

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG

43

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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062720 5324760

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
ACTAGTCGAC ATGGATTTWC AGGTGCAGAT TWTCAGCTTC

40

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
ACTAGTCGAC ATGAGGTKCY YTGYSAGYT YCTGRGG

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
ACTAGTCGAC ATGGGCWTCA AGATGGAGTC ACAKWYYCWG G

41

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
ACTAGTCGAC ATGTGGGGAY CTKTTTYCMM TTTTCAATT G

41

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
ACTAGTCGAC ATGGTRTCCW CASCTCAGTT CCTTG

35

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(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACTAGTCGAC ATGTATATAT GTTTGTTGTC TATTTCT

37

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACTAGTCGAC ATGGAAGCCC CAGCTCAGCT TCTCTTC

38

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGATCCCGGG TGGATGGTGG GAAGATG

27

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTAGTCGAC ATGAAATGCA GCTGGGTCAT STTCTTC

37

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:

0914485 071396

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTAGTCGAC ATGGGATGGA GCTRTATCAT SYTCTT

36

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACTAGTCGAC ATGAAGWTGT GGTTAACTG GGTTTTT

37

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACTAGTCGAC ATGRACCTTG GGYTCAGCTT GRTTT

35

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTAGTCGAC ATGGACTCCA GGCTCAATTT AGTTTTCTT

40

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACTAGTCGAC ATGGCTGTCY TRGSGCTRCT CTTCTGC

37

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT

36

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACTAGTCGAC ATGAGAGTGC TGATTCTTTT GTG

33

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACTAGTCGAC ATGGMTTGGG TGTGGAMCTT GCTATTCCTG

40

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

09114235 071398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACTAGTCGAC ATGGGCAGAC TTACATTCTC ATTCCTG

37

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCCCGGG CCAGTGGATA GACAGATG

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..393

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG	GAG	TCA	GAC	ACA	CTC	CTG	CTA	TGG	GTA	CTG	CTG	CTC	TGG	GTT	CCA	48
Met	Glu	Ser	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro	
1				5				10						15		
GGT	TCC	ACT	GGT	GAC	ATT	GTG	CTG	ACA	CAG	TCT	CCT	GCT	TCC	TTA	GGT	96
Gly	Ser	Thr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Gly	
			20				25						30			
GTA	TCT	CTG	GGG	CAG	AGG	GCC	ACC	ATC	TCA	TGC	AGG	GCC	AGC	AAA	AGT	144
Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Lys	Ser	
			35				40					45				
GTC	AGT	ACA	TCT	GGC	TAT	AGT	TAT	ATG	CAC	TGG	TAC	CAA	CAG	AAA	CCA	192
Val	Ser	Thr	Ser	Gly	Tyr	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	
			50				55				60					
GGA	CAG	ACA	CCC	AAA	CTC	CTC	ATC	TAT	CTT	GCA	TCC	AAC	CTA	GAA	TCT	240
Gly	Gln	Thr	Pro	Lys	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Asn	Leu	Glu	Ser	
			65		70				75					80		
GGG	GTC	CCT	GCC	AGG	TTC	AGT	GGC	AGT	GGG	TCT	GGG	ACA	GAC	TTC	ACC	288
Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	
				85					90					95		

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CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT	336
Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys	
100 105 110	
CAG CAC AGT AGG GAG AAT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG	384
Gln His Ser Arg Glu Asn Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu	
115 120 125	
GAA ATA AAA	393
Glu Ile Lys	
130	

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Glu	Ser	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5					10					15	
Gly	Ser	Thr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Gly
			20					25					30		
Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Lys	Ser
		35					40					45			
Val	Ser	Thr	Ser	Gly	Tyr	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro
	50					55					60				
Gly	Gln	Thr	Pro	Lys	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Asn	Leu	Glu	Ser
65					70					75				80	
Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
				85				90					95		
Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys
			100					105					110		
Gln	His	Ser	Arg	Glu	Asn	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu
		115					120					125			
Glu	Ile	Lys													
130															

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..405

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(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG GGA TGG AGC GGG ATC TTT CTC TTC CTT CTG TCA GGA ACT GCA GGT	48
Met Gly Trp Ser Gly Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly	
1 5 10 15	
GTC CAC TCT GAG ATC CAG CTG CAG CAG TCT GGA CCT GAG CTG ATG AAG	96
Val His Ser Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys	
20 25 30	
CCT GGG GCT TCA GTG AAG ATA TCC TGC AAG GCT TCT GGT TAC TCA TTC	144
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe	
35 40 45	
ACT AGC TAT TAC ATA CAC TGG GTG AAG CAG AGC CAT GGA AAG AGC CTT	192
Thr Ser Tyr Tyr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu	
50 55 60	
GAG TGG ATT GGA TAT ATT GAT CCT TTC AAT GGT GGT ACT AGC TAC AAC	240
Glu Trp Ile Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn	
65 70 75 80	
CAG AAA TTC AAG GGC AAG GCC ACA TTG ACT GTT GAC AAA TCT TCC AGC	288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser	
85 90 95	
ACA GCC TAC ATG CAT CTC AGC AGC CTG ACA TCT GAG GAC TCT GCA GTC	336
Thr Ala Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val	
100 105 110	
TAT TAC TGT GCA AGG GGG GGT AAC CGC TTT GCT TAC TGG GGC CAA GGG	384
Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly	
115 120 125	
ACT CTG GTC ACT GTC TCT GCA	405
Thr Leu Val Thr Val Ser Ala	
130 135	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Gly Trp Ser Gly Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15
Val His Ser Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys
20 25 30
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
35 40 45
Thr Ser Tyr Tyr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu
50 55 60

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Glu Trp Ile Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn
65 70 75 80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85 90 95
Thr Ala Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly
115 120 125
Thr Leu Val Thr Val Ser Ala
130 135

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..381

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATG GTG TCC TCA GCT CAG TTC CTT GGT CTC CTG TTG CTC TGT TTT CAA	48
Met Val Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln	
1 5 10 15	
GGT ACC AGA TGT GAT ATC CAG ATG ACA CAG ACT ACA TCC TCC CTG TCT	96
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser	
20 25 30	
GCC TCT CTG GGA GAC AGA GTC ACC ATC AGT TGC AGG GCA AGT CAG GAC	144
Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp	
35 40 45	
ATT AGC AGT TAT TTA AAC TGG TAT CAG CAG AAA CCA GAT GGA ACT ATT	192
Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Ile	
50 55 60	
AAA CTC CTG ATC TAC TAC ACA TCA AGA TTA CAC TCA GGA GTC CCA TCA	240
Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser	
65 70 75 80	
AGG TTC AGT GGC AGT GGG TCT GGA ACA GAT TAT TCT CTC ACC ATT AAC	288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn	
85 90 95	
AAC CTG GAG CAA GAA GAC ATT GCC ACT TAC TTT TGC CAA CAG GGT AAC	336
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn	
100 105 110	
ACG CTT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAT	381
Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Asn	
115 120 125	

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Val	Ser	Ser	Ala	Gln	Phe	Leu	Gly	Leu	Leu	Leu	Cys	Phe	Gln		
1				5				10					15			
Gly	Thr	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	
			20					25					30			
Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	
		35					40					45				
Ile	Ser	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Ile	
	50					55					60					
Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser	
	65				70					75					80	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Asn	
				85					90					95		
Asn	Leu	Glu	Gln	Glu	Asp	Ile	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Gly	Asn	
			100					105					110			
Thr	Leu	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Asn		
		115					120					125				

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..411

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATG	AGA	GTG	CTG	ATT	CTT	TTG	TGG	CTG	TTC	ACA	GCC	TTT	CCT	GGT	ATC	48
Met	Arg	Val	Leu	Ile	Leu	Leu	Trp	Leu	Phe	Thr	Ala	Phe	Pro	Gly	Ile	
1				5				10					15			
CTG	TCT	GAT	GTG	CAG	CTT	CAG	GAG	TCG	GGA	CCT	GTC	CTG	GTG	AAG	CCT	96
Leu	Ser	Asp	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Val	Leu	Val	Lys	Pro	
			20					25					30			

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TCT CAG TCT CTG TCC CTC ACC TGC ACT GTC ACT GGC TAC TCA ATC ACC	144
Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr	
35 40 45	
AGT GAT CAT GCC TGG AGC TGG ATC CGG CAG TTT CCA GGA AAC AAA CTG	192
Ser Asp His Ala Trp Ser Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu	
50 55 60	
GAG TGG ATG GGC TAC ATA AGT TAC AGT GGT ATC ACT ACC TAC AAC CCA	240
Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro	
65 70 75 80	
TCT CTC AAA AGT CGA ATC TCT ATC ACT CGA GAC ACA TCC AAG AAC CAG	288
Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln	
85 90 95	
TTC TTC CTA CAG TTG AAT TCT GTG ACT ACT GGG GAC ACG TCC ACA TAT	336
Phe Phe Leu Gln Leu Asn Ser Val Thr Thr Gly Asp Thr Ser Thr Tyr	
100 105 110	
TAC TGT GCA AGA TCC CTA GCT CGG ACT ACG GCT ATG GAC TAC TGG GGT	384
Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly	
115 120 125	
CAA GGA ACC TCA GTC ACC GTC TCC TCA	411
Gln Gly Thr Ser Val Thr Val Ser Ser	
130 135	

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Arg Val Leu Ile Leu Leu Trp Leu Phe Thr Ala Phe Pro Gly Ile	
1 5 10 15	
Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Val Leu Val Lys Pro	
20 25 30	
Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr	
35 40 45	
Ser Asp His Ala Trp Ser Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu	
50 55 60	
Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro	
65 70 75 80	
Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln	
85 90 95	
Phe Phe Leu Gln Leu Asn Ser Val Thr Thr Gly Asp Thr Ser Thr Tyr	
100 105 110	
Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly	
115 120 125	
Gln Gly Thr Ser Val Thr Val Ser Ser	
130 135	

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B5E F 20 5824T60

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..393

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATG GAG TCA GAC ACA CTC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA	48
Met Glu Ser Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro	
1 5 10 15	
GGT TCC ACA GGT GAC ATT GTG TTG ATC CAA TCT CCA GCT TCT TTG GCT	96
Gly Ser Thr Gly Asp Ile Val Leu Ile Gln Ser Pro Ala Ser Leu Ala	
20 25 30	
GTG TCT CTA GGG CAG AGG GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT	144
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser	
35 40 45	
GTT GAT AGT TAT GGC AAT AGT TTT ATG CAC TGG TAC CAG CAG AAA CCA	192
Val Asp Ser Tyr Gly Asn Ser Phe Met His Trp Tyr Gln Gln Lys Pro	
50 55 60	
GGA CAG CCA CCC AAA CTC CTC ATC TAT CGT GCA TCC AAC CTA GAA TCT	240
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser	
65 70 75 80	
GGG ATC CCT GCC AGG TTC AGT GGC AGT GGG TCT AGG ACA GAC TTC ACC	288
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr	
85 90 95	
CTC ACC ATT AAT CCT GTG GAG GCT GAT GAT GTT GCA ACC TAT TAC TGT	336
Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys	
100 105 110	
CAG CAA AGT AAT GAG GAT CCT CCC ACG TTC GGT GCT GGG ACC AAG CTG	384
Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu	
115 120 125	
GAG CTG AAA	393
Glu Leu Lys	
130	

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Glu Ser Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Ile Val Leu Ile Gln Ser Pro Ala Ser Leu Ala
 20 25 30
 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
 35 40 45
 Val Asp Ser Tyr Gly Asn Ser Phe Met His Trp Tyr Gln Gln Lys Pro
 50 55 60
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser
 65 70 75 80
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr
 85 90 95
 Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys
 100 105 110
 Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu
 115 120 125
 Glu Leu Lys
 130

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..417

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATG GGA TGG AGC GGG GTC TTT ATC TTC CTC CTG TCA GTA ACT GCA GGT	48
Met Gly Trp Ser Gly Val Phe Ile Phe Leu Leu Ser Val Thr Ala Gly	
1 5 10 15	
GTC CAC TCC CAG GTT CAA TTG CAG CAG TCT GGA GCT GAG TTG ATG AAG	96
Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys	
20 25 30	
CCT GGG GCC TCA GTC AAG ATC TCC TGC AAG GCT ACT GGC TAC ACA TTC	144
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe	
35 40 45	
AGT AGT TAT TGG ATA GTG TGG ATA AAG CAG AGG CCT GGA CAT GGC CTT	192
Ser Ser Tyr Trp Ile Val Trp Ile Lys Gln Arg Pro Gly His Gly Leu	
50 55 60	

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GAG	TGG	ATT	GGA	GAG	ATT	TTA	CCT	GGA	ACC	GGT	AGT	ACT	AAC	TAC	AAT	240
Glu	Trp	Ile	Gly	Glu	Ile	Leu	Pro	Gly	Thr	Gly	Ser	Thr	Asn	Tyr	Asn	
65					70					75					80	
GAG	AAA	TTC	AAG	GGC	AAG	GCC	ACA	TTC	ACT	GCA	GAT	ACA	TCT	TCC	AAC	288
Glu	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Ser	Asn	
				85					90					95		
ACA	GCC	TAC	ATG	CAA	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	TCT	GCC	GTC	336
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	
			100					105					110			
TAT	TAC	TGT	GCA	AGT	CTA	GAC	AGC	TCG	GGC	TAC	TAT	GCT	ATG	GAC	TAT	384
Tyr	Tyr	Cys	Ala	Ser	Leu	Asp	Ser	Ser	Gly	Tyr	Tyr	Ala	Met	Asp	Tyr	
		115					120					125				
TGG	GGT	CAA	GGA	ACC	TCA	GTC	ACC	GTC	TCC	TCA						417
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser						
130						135										

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Gly	Trp	Ser	Gly	Val	Phe	Ile	Phe	Leu	Leu	Ser	Val	Thr	Ala	Gly
1				5					10					15	
Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Met	Lys
			20					25					30		
Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Thr	Gly	Tyr	Thr	Phe
		35					40					45			
Ser	Ser	Tyr	Trp	Ile	Val	Trp	Ile	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu
	50					55				60					
Glu	Trp	Ile	Gly	Glu	Ile	Leu	Pro	Gly	Thr	Gly	Ser	Thr	Asn	Tyr	Asn
65					70					75					80
Glu	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Ser	Asn
				85					90					95	
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
			100					105					110		
Tyr	Tyr	Cys	Ala	Ser	Leu	Asp	Ser	Ser	Gly	Tyr	Tyr	Ala	Met	Asp	Tyr
		115					120					125			
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser					
130						135									

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..381

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATG	GTG	TCC	ACA	CCT	CAG	TTC	CTT	GGT	CTC	CTG	TTG	ATC	TGT	TTT	CAA	48
Met	Val	Ser	Thr	Pro	Gln	Phe	Leu	Gly	Leu	Leu	Leu	Ile	Cys	Phe	Gln	
1				5					10					15		
GGT	ACC	AGA	TGT	GAT	ATC	CAG	ATG	ACA	CAG	ACT	ACA	TCC	TCC	CTG	TCT	96
Gly	Thr	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	
			20					25					30			
GCC	TCT	CTG	GGA	GAC	AGA	GTC	ACC	ATC	AGT	TGC	AGG	GCA	AGT	CAG	GAC	144
Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	
			35				40					45				
ATT	AGT	AAT	TAT	TTA	AAC	TGG	TAT	CAA	CAG	AAA	CCA	GAT	GGA	ACT	GTT	192
Ile	Ser	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Val	
	50					55					60					
AAA	CTC	CTG	ATC	TAC	TAT	ACA	TCA	AGA	TTA	CAC	TCA	GGA	GTC	CCA	TCA	240
Lys	Leu	Leu	Ile	Tyr	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser		
65				70				75						80		
AGG	TTC	AGT	GGC	AGT	GGG	TCT	GGA	ACA	GAT	TAT	TCT	CTC	ACC	ATT	AGC	288
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	
				85				90						95		
AAC	CTG	GAG	CAA	GAA	GAT	ATT	GCC	AGT	TAC	TTT	TGC	CAA	CAG	GGT	TAT	336
Asn	Leu	Glu	Gln	Glu	Asp	Ile	Ala	Ser	Tyr	Phe	Cys	Gln	Gln	Gly	Tyr	
			100				105					110				
ACG	CCT	CCG	TGG	ACG	TTC	GGT	GGA	GGC	ACC	AAG	TTG	GAA	ATC	AAA		381
Thr	Pro	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
		115				120						125				

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Val	Ser	Thr	Pro	Gln	Phe	Leu	Gly	Leu	Leu	Leu	Ile	Cys	Phe	Gln
1				5					10					15	
Gly	Thr	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser
			20					25					30		
Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp
			35				40					45			
Ile	Ser	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Val
	50					55					60				

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Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
65 70 75 80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
85 90 95
Asn Leu Glu Gln Glu Asp Ile Ala Ser Tyr Phe Cys Gln Gln Gly Tyr
100 105 110
Thr Pro Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
115 120 125

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..402

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG GAG CTG GAT CTT TAT CTT ATT CTG TCA GTA ACT TCA GGT GTC TAC	48
Met Glu Leu Asp Leu Tyr Leu Ile Leu Ser Val Thr Ser Gly Val Tyr	
1 5 10 15	
TCA CAG GTT CAG CTC CAG CAG TCT GGG GCT GAG CTG GCA AGA CCT GGG	96
Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly	
20 25 30	
GCT TCA GTG AAG TTG TCC TGC AAG GCT TCT GGC TAC ACC TTT ACT AAC	144
Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn	
35 40 45	
TAC TGG GTG CAG TGG GTA AAA CAG AGG CCT GGA CAG GGT CTG GAA TGG	192
Tyr Trp Val Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp	
50 55 60	
ATT GGG TCT ATT TAT CCT GGA GAT GGT GAT ACT AGG AAC ACT CAG AAG	240
Ile Gly Ser Ile Tyr Pro Gly Asp Gly Asp Thr Arg Asn Thr Gln Lys	
65 70 75 80	
TTC AAG GGC AAG GCC ACA TTG ACT GCA GAT AAA TCC TCC ATC ACA GCC	288
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ile Thr Ala	
85 90 95	
TAC ATG CAA CTC ACC AGC TTG GCA TCT GAG GAC TCT GCG GTC TAT TAC	336
Tyr Met Gln Leu Thr Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr	
100 105 110	
TGT GCA AGA TCG ACT GGT AAC CAC TTT GAC TAC TGG GGC CAA GGC ACC	384
Cys Ala Arg Ser Thr Gly Asn His Phe Asp Tyr Trp Gly Gln Gly Thr	
115 120 125	

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ACT CTC ACA GTC TCC TCA
Thr Leu Thr Val Ser Ser
130

402

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Glu Leu Asp Leu Tyr Leu Ile Leu Ser Val Thr Ser Gly Val Tyr
1 5 10 15
Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly
20 25 30
Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn
35 40 45
Tyr Trp Val Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp
50 55 60
Ile Gly Ser Ile Tyr Pro Gly Asp Gly Asp Thr Arg Asn Thr Gln Lys
65 70 75 80
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ile Thr Ala
85 90 95
Tyr Met Gln Leu Thr Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr
100 105 110
Cys Ala Arg Ser Thr Gly Asn His Phe Asp Tyr Trp Gly Gln Gly Thr
115 120 125
Thr Leu Thr Val Ser Ser
130

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ACAAAGCTTC CACCATGGAG TCAGACACAC TCCTG

35

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGCTAAGCTT CCACCATGGG ATGGAGCGGG ATCTTT

36

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTGGATCCA CTCACGTTTT ATTTCCAGCT TGGTC

35

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTTGGATCCA CTCACCTGCA GAGACAGTTA CCAGAG

36

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTTGGATCCA CTCACGATTT ATTTCCAGCT TGGTC

35

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTTGGATCCA CTCACGTTTT ATTTCCAGCT TGGTC

35

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACAAAGCTTC CACCATGGTG TCCTCAGCTC AGTTCC

36

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TGTTAGATCT ACTCACCTGA GGAGACAGTG ACTGAGGTT

39

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTCTAAGCTT CCACCATGAG AGTGCTGATT CTTTTG

36

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TACGCAAACC GCCTCTC

17

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(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GAGTGCACCA TATGCGGT

18

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ACCGTGTCTG GCTACACCTT CACCAGCGAT CATGCCTGGA GCTGGGTGAG ACAGC

55

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGAGTGGATT GGATACATTA GTTATAGTGG AATCACAACC TATAATCCAT CTCTCAAATC

60

CAG

63

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TATTATTGTG CAAGATCCCT AGCTCGGACT ACGGCTATGG ACTACTGGGG TCAA

54

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(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTGACAATGC TGAGAGACAC CAGCAAG

27

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGTGTCCACT CCGATGTCCA ACTG

24

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGTCTTGAGT GGATGGGATA CATTAGT

27

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTGTCTGGCT ACTCAATTAC CAGCATCAT

29

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SECRET

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TGTAGAGCCA GCCAGGACAT CAGCAGTTAC CTGAACTGGT ACCAGCAG

48

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ATCTACTACA CCTCCAGACT GCACTCTGGT GTGCCAAGCA GA

42

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCTACTACT GCCAACAGGG TAACACGCTT CCATACACGT TCGGCCAAGG

50

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AGCGGTACCG ACTACACCTT CACCATC

27

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(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8..52

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 8..52

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 135..503

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 135..503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AAGCTTC ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT	49
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala	
1 5 10	
ACA GGTAAGGGGC TCACAGTAGC AGGCTTGAGG TCTGGACATA TATATGGGTG	102
Thr	
15	
ACAATGACAT CCACTTTGCC TTTCTCTCCA CA GGT GTC CAC TCC CAG GTC CAA	155
Gly Val His Ser Gln Val Gln	
1 5	
CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA CCT AGC CAG ACC CTG AGC	203
Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser	
10 15 20	
CTG ACC TGC ACC GTG TCT GGC TAC TCA ATT ACC AGC GAT CAT GCC TGG	251
Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp His Ala Trp	
25 30 35	
AGC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT GAG TGG ATT GGA TAC	299
Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Tyr	
40 45 50 55	
ATT AGT TAT AGT GGA ATC ACA ACC TAT AAT CCA TCT CTC AAA TCC AGA	347
Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu Lys Ser Arg	
60 65 70	
GTG ACA ATG CTG AGA GAC ACC AGC AAG AAC CAG TTC AGC CTG AGA CTC	395
Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu	
75 80 85	
AGC AGC GTG ACA GCC GCC GAC ACC GCG GTT TAT TAT TGT GCA AGA TCC	443
Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser	
90 95 100	

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CTA GCT CGG ACT ACG GCT ATG GAC TAC TGG GGT CAA GGC AGC CTC GTC 491
Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly Ser Leu Val
105 110 115

ACA GTC TCC TCA GGTGAGTCCT TACAACCTCT CTCTTCTATT CAGCTTAAAT 543
Thr Val Ser Ser
120

AGATTTTACT GCATTTGTTG GGGGGGAAAT GTGTGTATCT GAATTTTCAGG TCATGAAGGA 603

CTAGGGACAC CTTGGGAGTC AGAAAGGGTC ATTGGGAGCC CGGGCTGATG CAGACAGACA 663

TCCTCAGCTC CCAGACTTCA TGGCCAGAGA TTTATAGGGA TCC 706

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gly Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
1 5 10 15
Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser
20 25 30
Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg
35 40 45
Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr
50 55 60
Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys
65 70 75 80
Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
85 90 95
Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr
100 105 110
Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser
115 120

014425-074396

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 8..52

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 8..52

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 135..467

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 135..467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AAGCTTC ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT	49
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala	
1 5 10	
ACA GGTAAGGGGC TCACAGTAGC AGGCTTGAGG TCTGGACATA TATATGGGTG	102
Thr	
15	
ACAATGACAT CCACTTTGCC TTTCTCTCCA CA GGT GTC CAC TCC GAC ATC CAG	155
Gly Val His Ser Asp Ile Gln	
1 5	
ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG	203
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val	
10 15 20	
ACC ATC ACC TGT AGA GCC AGC CAG GAC ATC AGC AGT TAC CTG AAT TGG	251
Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp	
25 30 35	
TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG CTG ATC TAC TAC ACC	299
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr	
40 45 50 55	
TCC AGA CTG CAC TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT AGC	347
Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser	
60 65 70	
GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC	395
Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile	
75 80 85	
GCT ACC TAC TAC TGC CAA CAG GGT AAC ACG CTT CCA TAC ACG TTC GGC	443
Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly	
90 95 100	

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CAA GGG ACC AAG GTG GAA ATC AAA CGTGAGTAGA ATTTAAACTT TGCTTCCTCA 497
Gln Gly Thr Lys Val Glu Ile Lys
105 110

GTTGGATCC 506

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Gly Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
1 5 10 15
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
20 25 30
Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45
Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
65 70 75 80
Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn
85 90 95
Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..425

058270" 5324T60

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 12..425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AAGCTTCCAC C ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA	50
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr	
1 5 10	
GCT ACA GGT GTC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT	98
Ala Thr Gly Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	
15 20 25	
CTT GTG AGA CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GTG TCT GGC	146
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	
30 35 40 45	
TAC TCA ATT ACC AGC GAT CAT GCC TGG AGC TGG GTT CGC CAG CCA CCT	194
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	
50 55 60	
GGA CGA GGT CTT GAG TGG ATT GGA TAC ATT AGT TAT AGT GGA ATC ACA	242
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	
65 70 75	
ACC TAT AAT CCA TCT CTC AAA TCC AGA GTG ACA ATG CTG AGA GAC ACC	290
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	
80 85 90	
AGC AAG AAC CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC	338
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp	
95 100 105	
ACC GCG GTT TAT TAT TGT GCA AGA TCC CTA GCT CGG ACT ACG GCT ATG	386
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
110 115 120 125	
GAC TAC TGG GGT CAA GGC AGC CTC GTC ACA GTC TCC TCA GGTGAGTGA	435
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser	
130 135	
TCC	438

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
20 25 30	
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile	
35 40 45	

05E120" 5824T60

Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly
50 55 60
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn
65 70 75 80
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn
85 90 95
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp
115 120 125
Gly Gln Gly Ser Leu Val Thr Val Ser Ser
130 135

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 12..389

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 12..389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AAGCTTCCAC C ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA	50
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr	
1 5 10	
GCT ACA GGT GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC	98
Ala Thr Gly Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
15 20 25	
CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AGA GCC AGC	146
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
30 35 40 45	
CAG GAC ATC AGC AGT TAC CTG AAT TGG TAC CAG CAG AAG CCA GGA AAG	194
Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys	
50 55 60	
GCT CCA AAG CTG CTG ATC TAC TAC ACC TCC AGA CTG CAC TCT GGT GTG	242
Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val	
65 70 75	
CCA AGC AGA TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC	290
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr	
80 85 90	
ATC AGC AGC CTC CAG CCA GAG GAC ATC GCT ACC TAC TAC TGC CAA CAG	338
Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln	
95 100 105	

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GGT AAC ACG CTT CCA TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC 386
 Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 110 115 120 125

AAA CGTGAGTGGG TCC 402
 Lys

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
 20 25 30
 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile
 35 40 45
 Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 50 55 60
 Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg
 65 70 75 80
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
 85 90 95
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr
 100 105 110
 Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 115 120 125

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TAAGGATCCA CTCACCTGAG GAGACTGTGA CGAGGC

36

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
ATCAAGCTTC CACCATGGGA TGGAGCTGTA TC 32

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:
AATGGATCCA CTCACGTTTG ATTTCCACCT 30

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:
CATGCCTGGA GCTGGGTTTCG CCAGCCACCT GGA 33

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:
TCCAGGTGGC TGGCGAACCC AGCTCCAGGC ATG 33

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CAGCAGAAGC CAGGAAAGGC TCCAAAGCTG

30

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGCTTTGGA GCCTTTCCTG GCTTCTGCTG

30

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ACCTGTAGAG CCAGCAAGAG TGTTAGTACA TCTGGCTATA GTTATATGCA CTGGTACCAG
CAGAAG

60

66

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GCTGGCTCTA CAGGT

15

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAGCTGCTGA TCTACCTTCC ATCCACCCTG GAATCTGGTG TGCCAAGC

48

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GTAGATCAGC AGCTT

15

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCTACCTACT ACTGCCAGCA CAGTAGGGAG ACCCCATACA CGTTCGGC

48

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTGGCAGTAG GTAGC

15

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..401

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(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 12..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

AAGCTTCCAC C	ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA	50
	Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr	
	1 5 10	
GCT ACA GGT GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC	98	
Ala Thr Gly Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser		
	15 20 25	
CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AGA GCC AGC	146	
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser		
	30 35 40 45	
AAG AGT GTT AGT ACA TCT GGC TAT AGT TAT ATG CAC TGG TAC CAG CAG	194	
Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln		
	50 55 60	
AAG CCA GGA AAG GCT CCA AAG CTG CTG ATC TAC CTT GCA TCC AAC CTG	242	
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu		
	65 70 75	
GAA TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT AGC GGT ACC GAC	290	
Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp		
	80 85 90	
TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC GCT ACC TAC	338	
Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr		
	95 100 105	
TAC TGC CAG CAC AGT AGG GAG AAC CCA TAC ACG TTC GGC CAA GGG ACC	386	
Tyr Cys Gln His Ser Arg Glu Asn Pro Tyr Thr Phe Gly Gln Gly Thr		
	110 115 120 125	
AAG GTG GAA ATC AAA CGTGAGTGGGA TCC	414	
Lys Val Glu Ile Lys		
	130	

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
	20 25 30
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val	
	35 40 45
Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly	
	50 55 60

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Lys Ala Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly
65 70 75 80
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe
85 90 95
Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
100 105 110
His Ser Arg Glu Asn Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu
115 120 125
Ile Lys
130

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGTTATTCAT TCACTAGTTA TTACATACAC TGGGTTAGAC AGGCC

45

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGTGAATGAA TAACCGCTAG CTTTACA

27

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAGTGGGTGG GCTATATTGA TCCTTTCAAT GGTGGTACTA GCTATAATCA GAAGTTCAAG

60

GGCAGGGTT

69

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ATAGCCCACC CACTC

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

GGGGGTAACC GCTTTGCTTA CTGGGGACAG GGTACC

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

AGCAAAGCGG TTACCCCTC TGGCGCAGTA GTAGAC

36

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

CAAGGTTACC ATGACCGTGG ACACCTCTAC

30

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CACGGTCATG GTAACCTTGC CCTTGAACCTT

30

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGGCTCGAAT GGATTGGCTA TATTGATCCT

30

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

AGGATCAATA TAGCCAATCC ATTCGAGCCC

30

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTAAAACGAG GCQAGT

16

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(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AACAGCTATG ACCATGA

17

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 433 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 16..420

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 16..420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AAGCTTGCCG CCACC ATG GAC TGG ACC TGG CGC GTG TTT TGC CTG CTC GCC	51
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala	
1 5 10	
GTG GCT CCT GGG GCC CAC AGC CAG GTG CAA CTA GTG CAG TCC GGC GCC	99
Val Ala Pro Gly Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala	
15 20 25	
GAA GTG AAG AAA CCC GGT GCT TCC GTG AAA GTC AGC TGT AAA GCT AGC	147
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser	
30 35 40	
GGT TAT TCA TTC ACT AGT TAT TAC ATA CAC TGG GTT AGA CAG GCC CCA	195
Gly Tyr Ser Phe Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro	
45 50 55 60	
GGC CAA GGG CTC GAG TGG GTG GGC TAT ATT GAT CCT TTC AAT GGT GGT	243
Gly Gln Gly Leu Glu Trp Val Gly Tyr Ile Asp Pro Phe Asn Gly Gly	
65 70 75	
ACT AGC TAT AAT CAG AAG TTC AAG GGC AAG GTT ACC ATG ACC GTG GAC	291
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Val Thr Met Thr Val Asp	
80 85 90	
ACC TCT ACA AAC ACC GCC TAC ATG GAA CTG TCC AGC CTG CGC TCC GAG	339
Thr Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu	
95 100 105	

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GAC	ACT	GCA	TGC	TAC	TAC	TGC	GCC	AGA	GGG	GGT	AAC	CGC	TTT	GCT	TAC	387
Asp	Thr	Ala	Cys	Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Asn	Arg	Phe	Ala	Tyr	
110						115					120					
TGG	GGA	CAG	GGT	ACC	CTT	GTC	ACC	GTC	AGT	TCA	GGT	GAG	TGGA	TCC		433
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser						
125					130					135						

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met	Asp	Trp	Thr	Trp	Arg	Val	Phe	Cys	Leu	Leu	Ala	Val	Ala	Pro	Gly	
1				5					10					15		
Ala	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	
		35					40					45				
Thr	Ser	Tyr	Tyr	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
	50					55					60					
Glu	Trp	Val	Gly	Tyr	Ile	Asp	Pro	Phe	Asn	Gly	Gly	Thr	Ser	Tyr	Asn	
65					70					75					80	
Gln	Lys	Phe	Lys	Gly	Lys	Val	Thr	Met	Thr	Val	Asp	Thr	Ser	Thr	Asn	
				85					90						95	
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Cys	
			100					105					110			
Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Asn	Arg	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	
		115					120					125				
Thr	Leu	Val	Thr	Val	Ser	Ser										
		130			135											

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16..420

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 16..420

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AAGCTT	GGCCG	CCACC	ATG	GAC	TGG	ACC	TGG	CGC	GTG	TTT	TGC	CTG	CTC	GCC		51
			Met	Asp	Trp	Thr	Trp	Arg	Val	Phe	Cys	Leu	Leu	Ala		
			1				5					10				
GTG	GCT	CCT	GGG	GCC	CAC	AGC	CAG	GTG	CAA	CTA	GTG	CAG	TCC	GGC	GCC	99
Val	Ala	Pro	Gly	Ala	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	
		15					20					25				
GAA	GTG	AAG	AAA	CCC	GGT	GCT	TCC	GTG	AAA	GTC	AGC	TGT	AAA	GCT	AGC	147
Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	
	30					35					40					
GGT	TAT	TCA	TTC	ACT	AGT	TAT	TAC	ATA	CAC	TGG	GTT	AGA	CAG	GCC	CCA	195
Gly	Tyr	Ser	Phe	Thr	Ser	Tyr	Tyr	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	
	45				50					55					60	
GGC	CAA	GGG	CTC	GAA	TGG	ATT	GGC	TAT	ATT	GAT	CCT	TTC	AAT	GGT	GGT	243
Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asp	Pro	Phe	Asn	Gly	Gly	
				65					70					75		
ACT	AGC	TAT	AAT	CAG	AAG	TTC	AAG	GGC	AAG	GTT	ACC	ATG	ACC	GTG	GAC	291
Thr	Ser	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Val	Thr	Met	Thr	Val	Asp	
			80					85					90			
ACC	TCT	ACA	AAC	ACC	GCC	TAC	ATG	GAA	CTG	TCC	AGC	CTG	CGC	TCC	GAG	339
Thr	Ser	Thr	Asn	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	
		95					100					105				
GAC	ACT	GCA	GTC	TAC	TAC	TGC	GCC	AGA	GGG	GGT	AAC	CGC	TTT	GCT	TAC	387
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Asn	Arg	Phe	Ala	Tyr	
	110					115					120					
TGG	GGA	CAG	GGT	ACC	CTT	GTC	ACC	GTC	AGT	TCA	GGTGAGTGGGA TCC					433
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser						
	125				130					135						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met	Asp	Trp	Thr	Trp	Arg	Val	Phe	Cys	Leu	Leu	Ala	Val	Ala	Pro	Gly
1				5					10					15	
Ala	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			20					25					30		
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe
		35					40					45			
Thr	Ser	Tyr	Tyr	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
	50					55					60				
Glu	Trp	Ile	Gly	Tyr	Ile	Asp	Pro	Phe	Asn	Gly	Gly	Thr	Ser	Tyr	Asn
65					70					75					80
Gln	Lys	Phe	Lys	Gly	Lys	Val	Thr	Met	Thr	Val	Asp	Thr	Ser	Thr	Asn
				85					90					95	

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly
 115 120 125
 Thr Leu Val Thr Val Ser Ser
 130 135

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GATAAGCTTG CCGCCACCAT GGACTGGACC TGGAGGGTCT TCTTCTTGCT GGCTGTAGCT 60
 CCAGGTGCTC ACTCCCAGGT GCAGCTTGTTG 90

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CACTCCCAGG TGCAGCTTGT GCAGTCTGGA GCTGAGGTGA AGAAGCCTGG GGCCTCAGTG 60
 AAGGTTTCCT GCAAGGCTTC TGGATACTCA 90

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TGCAAGGCTT CTGGATACTC ATTCAGTAGT TATTACATAC ACTGGGTGCG CCAGGCCCCC 60
 GGACAAAGGC TTGAGTGGAT GGGATATATT 90

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CTTGAGTGGA TGGGATATAT TGACCCTTTC AATGGTGGTA CTAGCTATAA TCAGAAGTTC 60
AAGGGCAGAG TCACCATTAC CGTAGACACA 90

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GTCACCATTA CCGTAGACAC ATCCGCGAGC ACAGCCTACA TGGAGCTGAG CAGCCTGAGA 60
TCTGAAGACA CGGCTGTGTA TTACTGTGCG 90

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ACGGCTGTGT ATTACTGTGC GAGAGGGGGT AACCGCTTTG CTTACTGGGG CCAGGGAACC 60
CTGGTCACCG TCTCCTCAGG TGAGTGGATC CGAC 94

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GATAAGCTTG CCGCC 15

09114285-071398

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTCGGATCCA CTCAC

15

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16..420

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 16..420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AAGCTTGCCG CCACC	ATG GAC TGG ACC TGG AGG GTC TTC TTC TTG CTG GCT	51
	Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala	
	1 5 10	
GTA GCT CCA GGT GCT CAC TCC CAG GTG CAG CTT GTG CAG TCT GGA GCT	99	
Val Ala Pro Gly Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala		
15 20 25		
GAG GTG AAG AAG CCT GGG GCC TCA GTG AAG GTT TCC TGC AAG GCT TCT	147	
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser		
30 35 40		
GGA TAC TCA TTC ACT AGT TAT TAC ATA CAC TGG GTG CGC CAG GCC CCC	195	
Gly Tyr Ser Phe Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro		
45 50 55 60		
GGA CAA AGG CTT GAG TGG ATG GGA TAT ATT GAC CCT TTC AAT GGT GGT	243	
Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asp Pro Phe Asn Gly Gly		
65 70 75		
ACT AGC TAT AAT CAG AAG TTC AAG GGC AGA GTC ACC ATT ACC GTA GAC	291	
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp		
80 85 90		
ACA TCC GCG AGC ACA GCC TAC ATG GAG CTG AGC AGT CTG AGA TCT GAA	339	
Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu		
95 100 105		

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GAC ACG GCT GTG TAT TAC TGT GCG AGA GGG GGT AAC CGC TTT GCT TAC 387
 Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr
 110 115 120

TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA GGTGAGTGGG TCC 433
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 125 130 135

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
 1 5 10 15
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
 35 40 45
 Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
 50 55 60
 Glu Trp Met Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly
 115 120 125
 Thr Leu Val Thr Val Ser Ser
 130 135

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AGGCTTGAGT GGATTGGATA TATTGAC

27

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs

09144285-071398

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

AAGTTCAAGG GCAAGGTCAC CATTACC

27

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GGTGCTTCCG TGAAAGTCAG CTGTAAAGCT

30

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

AGCTTTACAG CTGACTTTCA CGGAAGCACC

30

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

0011425-071399

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Tyr Thr Ser Arg Leu His Ser
1 5

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Gln Gln Gly Asn Thr Leu Pro Tyr Thr
1 5

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys
20

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

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(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1 5 10 15
Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys
 20 25 30

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
 1 5 10 15
Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys
 20 25 30

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

0914285-071398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ser Asp His Ala Trp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Thr Phe Thr
20 25 30

0914285-04398

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg
1 5 10 15
Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Thr Phe Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Met Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Ala Ser Asn Leu Glu Ser
1 5

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Gln His Ser Arg Glu Asn Pro Tyr Thr
1 5

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

001435-01398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys
 20

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15
Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys
 20 25 30

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids

001425-0139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

(2) INFORMATION FOR SEQ ID NO:144:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gly

(2) INFORMATION FOR SEQ ID NO:145:

(xi) SEQUENCE DESCRIPTION: SEQ

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Arg Val Thr Met Thr Leu Asp Thr Ser Thr Asn Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids

001425-0133

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Lys	Val	Thr	Met	Thr	Val	Asp	Thr	Ser	Thr	Asn	Thr	Ala	Tyr	Met	Glu
1					5				10					15	
Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly
1				5					10				

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

09114285 1071398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Lys Val Thr Ile Thr Val Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

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